E117A

P-[07]-TV

TH-[07]-IR ODE-GGFINET

VEG-128

ACHABIS-[38]-EYKLINA RVHADIR-[061-"

#AR#S~[05]-Y

\*DIR-[06]-YHEDYG YITQ-[07]-LTID YYTT-[17]-TYKDN-FILK-[10]-YHODF-

F-[11]-YIED S-[06]-YIRC 

GL---SSFESSR

VOTIN----PIASSABCVEW-[12]-14

SIRG-277

**E**-100 **16**-94

NGT-AVGERYS-VP---IAL YGT-AVNERKVQ-NGFS-RTI NGT-AVNERIG-TNRM-RIF NGT-AVNERIVG-KGKR-RPIN

RRETK----SYR

Figure 1A

in

Mutations

RAD53

H88A

NTD-[15]-IDEDEGPAK---I

R70A

DNR-----SINGPANGARVD-----SAVILHI

DNR-----SINGPANGARVD-----AALITHI

DTK-----SINGPANGARVD-----AALITHI

DTK-----SINGPANGARVD-----AALITHI

DYK-----SINGPANGARVG----EWD-N

DNR-----SISGPATANHORTS-[08]-YP-ISI

DNG-----SISGPATANHORTS-[08]-YP-ISI

DNG-----SISGPATANHARPYQ----EWQ-AI

DNG----SINGPANGARVD-INS-HP---RQ-QI

II-------GRNGARVDDIRVE-RGNT-VP-ISI

DNG-----SINGPANGARVD------SAVDA

DNG-----SINGPANGARVD-----SAVDA

LVAEEPLISONTKQSHGKTIQ [07] FVIDAI

HEAVIV - [06] - VIC HEAVIV - [06] - EIG NEACIS - [08] - VIC NEACIS - [08] - VIC HECCEY - [07] - FIC

**G-133** 

MGOKVE-KNS.. TERA-KNSR-TIL

REIR----SAVT

0.3-vs.HGRNTD-[18]-VNIDLIGPAK---VVS 118-ITVGRNSS-Q----CDVALCKNK---FIS 66-WTEGRNPA-----CDYHJGNIS---RUSS 60-WGEGRHKS-----CEVVING----PRVS 308-TRIGRLHD-----NDIVIDSAN----VSS 228-VRIGRAND-----NDIVIDEVI-----PVA [22] QVRSDNGNFDSRVĀ PVT-[17]-QVRPDNGNFDSRV YTE-[09]-PDQYHPVVFKSKV YTE-[09]-PEQYHPVVFKSKV

99-LK 189-II 295-LV

MtuCY04C12.31 Mtuembr ydr200c ylr283w yhr115c yn1116w

ScRad53 (FHA1)

SpCds1

v1r183c

ScFkh2

ScFkh1

SpDma1

MtuCY10H4.20C

MtuCY1A11.16C AnaCYAD SCFh11

Mtucy10H4.19C ydr501w AnaFrah Scbun1

HsNibrin Syncyaa Dachk2

H<sub>s</sub>Chk<sub>2</sub>

SynMCRB MENTE

CeZK632.2 791081W HsKi-67 Atkapp ScMek1

ScRad53 (FHA2)

vlr016c

BOX

1/8

16-137 16-518 17-89 17-89 17-374

HDEDITORG-273 PRDEDITORG-379 USNNDIRORG-137

G-292

NGPJJVNTELYG-KGKR-RPI NGVIJVJGAFQR-RGAPALQI NGTYTQRRFTK----SYRI

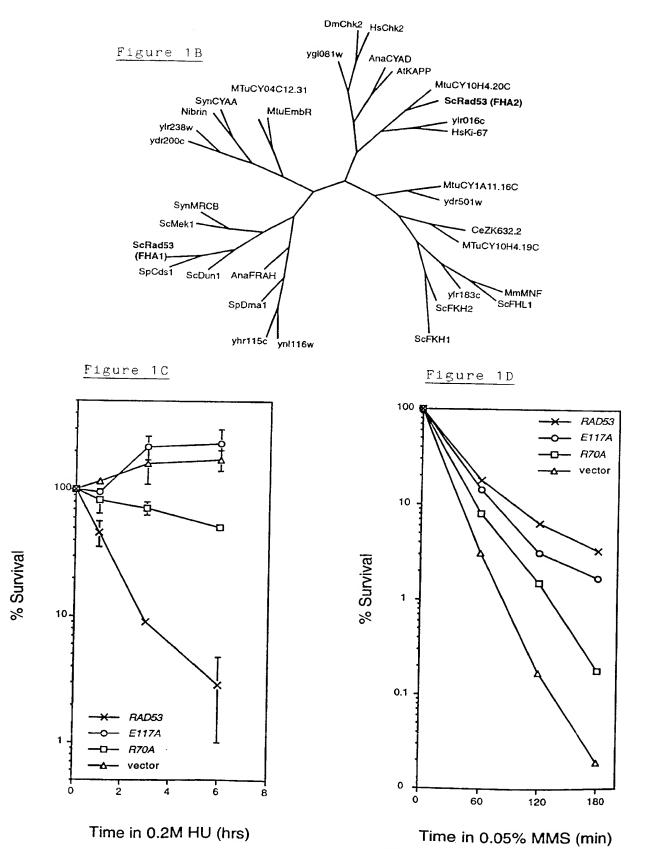
BOX

O BOX

М

Q - [10] - Y

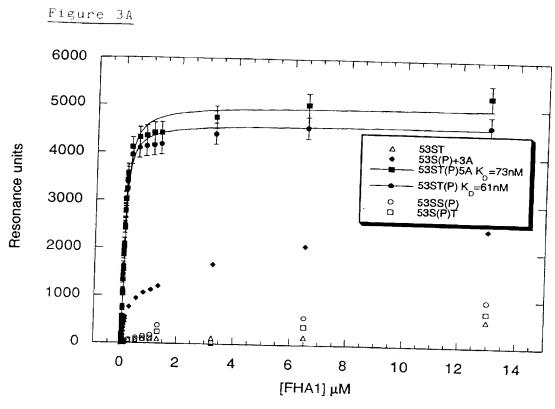
BOX

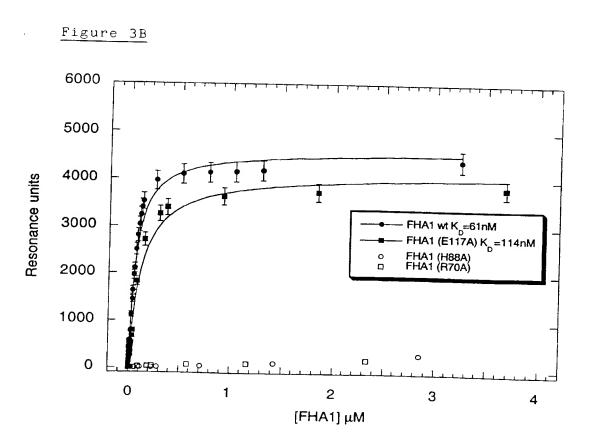


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## Figure 2

APPLSQETFSDLWKL	ST
APPLS(P)QETFSDLWKL	S(P)T
APPLSQET(P)FSDLWKL	ST(P)
APPLAQET(P)FSDLWKL	ST(P)-3A
APPLS <b>A</b> ET(P)FSDLWKL	ST(P)-2A
APPLSQAT(P)FSDLWKL	ST(P)-1A
APPLSQET(P)ASDLWKL	ST(P)+1A
APPLSQET(P)F <b>A</b> DLWKL	ST(P)+2A
APPLSQET(P)FS <b>A</b> LWKL	ST(P)+3A
ALAAAT(P)AADAAL	ST(P)5A
AL <b>AAADAA</b> DAAL	SDŠÁ
APPLSQE <b>S(P)</b> FSDLWKL	SS(P)
GGKKATQSQEY	H2AS
GGKKATQS(P)QEY	H2AS(P)





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### Figure 4

# Growth factor signalling

# 1. Ligand binding SH2 2. Receptor autophosphorylation on Tyrosine 4. Signal amplification and signal diversification

# DNA damage signalling

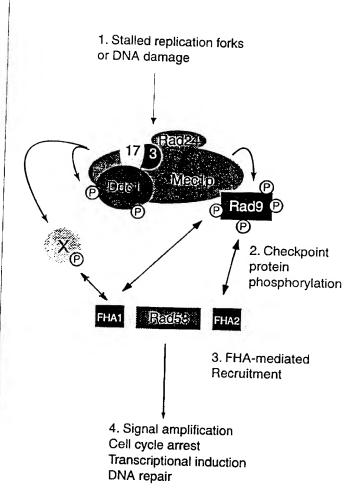
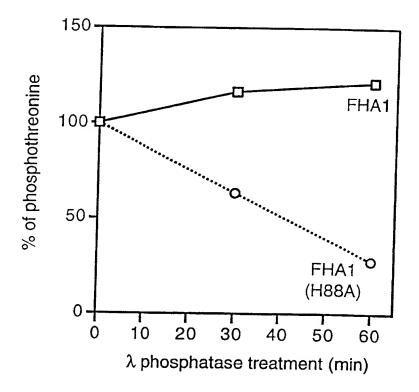
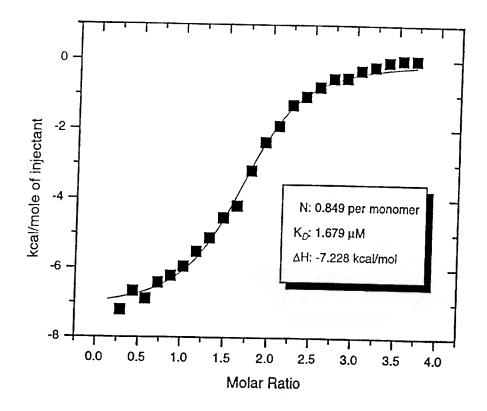


Figure 5



936955

Figure 6



PCT/GB00/01024

8/8

Figure 7

A

T: Biotin-SGSYSQETXXXLL T(P): Biotin-SGSYSQET(P)XXXLL

